

```
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mic:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodont:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriopl:*
17: sp_archeo:*
```

Result No.	Score	Query Match	Length	DB ID	Description
1	1252	63.6	352	6 Q93NC2	Q95nc2 callicebus
2	1244	63.1	339	6 Q97UV8	Q97uv8 saquinus
3	1244	63.1	339	6 Q97OT3	Q97ot3 callithrix
4	1244	63.1	352	6 Q97MA0	Q97ma0 callicebus
5	1243	63.1	339	6 Q97AV5	Q97av5 saquinus
6	1243	63.1	352	6 Q97C4	Q97c4 atelopus geoffroyi
7	1240	62.9	339	6 Q97UW0	Q97uw0 saquinus
8	1239	62.9	352	6 Q94Z99	Q97z99 atelopus sp
9	1238.5	62.9	339	6 Q97UV6	Q97uv6 saquinus
10	1238	62.8	339	6 Q97UW1	Q97uw1 saquinus
11	1237	62.8	339	6 Q97UV9	Q97uv9 saquinus
12	1236	62.7	339	6 Q97OR0	Q97or0 hylobates
13	1235	62.7	339	6 Q97SM3	Q97sm3 macacus fasciatus
14	1235	62.7	352	6 Q97776	Q97776 cercopithecus
15	1234	62.6	339	6 Q97UV5	Q97uv5 saquinus
16	1233	62.6	339	6 Q97UV7	Q97uv7 alouatta

ALIGNMENTS

OX RN RP RA RT RT RL DR DR DR DR DR DR DR DR DR KW SQ Qu Be Ma QY Db QY

Db	64	MTDIYLLNLAISDLEFLTVFPAWHAAGGDFGNTMCQFLTGLYFIGFGIFFLILT	123	QY	258	PYNIVILLNTFQEFFGLSNESTSOLDQATQVTERLGMTHCCINPILYAFVGKEKFRSLF- 316
Qy	136	IDRTLAIVAAVFAALKARTVTFGVVTSVTLVAVFASVPOUPTFRCQKESVYVGPF 195		Db	243	PYNIVILLNTYQEFFGLNCCSSSNRDLQAMQVTTETLGMTHCCINPILYAFVGKEKFRNYL 302
Db	124	IDRTLAIVAAVFAALKARTVTFGVVTSVTLVAVFASVPOUPTFRCQKESVYVGPF 183		Qy	317	----HIA 319
Qy	196	RG ---WNNFTIMRNLLGVLPLIMIVCYSGILKTLRCRNEKKRRAVRIFTIMV 251		Db	303	VFFQKHIA 310
Db	184	FGQTRFWKMLETLMVILGVLPLIMIVCYSGILKTLRCRNEKKRRAVRIFTIMV 243				RESULT 3
Qy	252	YFLWTPNIVILLNTFQEFFGLSNESTSOLDQATOVTETLGMTHCCINPILYAFVGK 311		Q9TQ73		PRELIMINARY;
Db	244	YFLWAPNIVILLNTYQEFFGLNCCSSSNRDLQAMQVTTETLGMTHCCINPILYAFVGK 303		AC	Q9TQ73;	PRELIMINARY;
Qy	312	FRSIF----HIA 319		DT	01-MAY-2000 (TREMBrel. 13, Created)	
Db	304	FRNLLVFFQKHIA 317		DT	01-MAY-2000 (TREMBrel. 13, Last sequence update)	
				DT	01-MAR-2002 (TREMBrel. 20, Last annotation update)	
				DE	C-C chemokine receptor 5 (Fragment).	
				DN	COR5	
				OS	Callithrix jacchus (Common marmoset).	
				OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Piatyrrini; Callitrichidae; Callithrix; NCBI_TaxID=5483;	
				OX		
				RN		
						SEQUENCE FROM N.A.
						RA
						Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
						RA
						Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
						"Sequences of the CCR5 genes from diverse simian and prosimian species.",
						RT
						Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
						DR
						EMBL; AF162021; AAD4776.1; -
						DR
						EMBL; AF161934; AAD47891.1; -
						DR
						EMBL; AF161935; AAD47692.1; -
						DR
						EMBL; AF161936; AAD47893.1; -
						DR
						EMBL; AF161937; AAD47694.1; -
						DR
						EMBL; AF161938; AAD47695.1; -
						DR
						EMBL; AF161939; AAD47696.1; -
						DR
						EMBL; AF161940; AAD47597.1; -
						DR
						EMBL; AF161941; AAD47700.1; -
						DR
						InterPro; IPR006923; BlueCu_1.
						DR
						InterPro; IPR00276; GPCR_Rhodopsin.
						DR
						PFam; PF0001; 7tm_1.
						DR
						PRINTS; PRO0237; GPCR_RHODOPSIN.
						DR
						PROSITE; PS00196; COPPER_BLUE; UNKNOWN_1.
						DR
						PROSITE; PS00237; G_PROTEIN_RECOP_F1_1; UNKNOWN_1.
						DR
						PROSITE; PS00237; G_PROTEIN_RECOP_F1_2; UNKNOWN_1.
						DR
						Receptor.
						KW
						FT
						NON_TER 1
						FT
						NON_TER 339 339 MW;
						SEQUENCE 339 AA; 39055 MW; C1313952E71B50C7 CRC64;
						Query Match 63.1%; Score 1244; DB 6; Length 339;
						Best Local Similarity 76.6%; Pred. No. 7.3e-302;
						Matches 236; Conservative 27; Mismatches 33; Indels 12; Gaps 3;
						3
						24 FDYDG--APCHKFDYKQIGAQOLLPLPLYSVLEFGVGNMVLVILJNCKLKCLTDYL 81
						Qy 82 YDIDGPSEPKDVKYQMGHLPLPYSMFLFGVGNMVLVILJNCKRSMDTDL 62
						Db 63 LNLAISDLFLITPLWAHSAAANEVFGNAKCKLFLGFLHGYEGGLFFILLTIDYL 141
						Qy 63 LNLAISDLFLITPLWAHZAGQDFGNTMCQFGTFLGFLFFGFFGFFILLTIDYL 122
						Db 122 IVHAYFALKARTVTFGVVTSVTLVAVFASVPOUPTFRCQKESVYVGPF 197
						Qy 123 IVHAYFALKARTVTFGVVTSVTLVAVFASVPOUPTFRCQKESVYVGPF 182
						Db 183 WKNFETLKVAVLGLVPLIMIVCYSGILKTLRCRNEKKRRAVRIFTIMVYFLFWA 242
						Qy 184 WNNFTIMRNLLGVLPLIMIVCYSGILKTLRCRNEKKRRAVRIFTIMVYFLFWA 242
						Db 183 WKNFETLKVAVLGLVPLIMIVCYSGILKTLRCRNEKKRRAVRIFTIMVYFLFWA 302
						Qy 184 PYNIVILLNTFQEFFGLSNESTSOLDQATOVTETLGMTHCCINPILYAFVGKEKFRSLF- 316
						Db 243 PYNIVILLNTYQEFFGLNCCSSSNRDLQAMQVTTETLGMTHCCINPILYAFVGKEKFRNYL 302

AC	Q95NC4;	RT	species.";
DT	01-DEC-2001 (TREMBrel. 19, Created)	RL	Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
DT	01-DEC-2001 (TREMBrel. 19, Last sequence update)	DR	EMBL; AF16927; AAU7684; 1.
DE	C-C chemokine receptor 5.	DR	InterPro; IPR00923; BlueCn_1.
GN	CCR5.	DR	InterPro; IPR00276; GPCR_Rhodpsn.
OS	Atelopus geoffroyi (Black-handed spider monkey), Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Atelinae; Atelopus [1].	DR	PRINTS; PRO0237; GPCRRIODPSN.
OC	Zhang Y., Ryder O.A., Zhang Y.; "Sequence comparison of the CCR5 gene in primates and primate phylogeny.";	DR	PROSITE; PS000196; COPPER_BLU; UNKNOWN_1.
RN	Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.	DR	PROSITE; PS00237; G_PROTEIN_RECV_F1_1; UNKNOWN_1.
RP	SEQUENCE FROM N.A.	DR	PROSITE; PS50262; G_PROTEIN_RECV_F1_2; 1.
RT	Zhang Y., Ryder O.A., Zhang Y.; "Sequence comparison of the CCR5 gene in primates and primate phylogeny.";	KW	Receptor.
RT	RT	FT	NON_TER
RN	RT	FT	1
RT	RT	SQ	SEQUENCE 339 AA; 339 MW; 7B358C5172B5C32 CRC64;
DR	EMBL; AF177885; AAK43368; 1;	Query Match	62.9%; Score 1240; DB 6; Length 339;
DR	InterPro; IPR00923; BlueCn_1.	Best Local Similarity	76.9%; Pred. No. 1..6e-101;
DR	InterPro; IPR00276; GPCR_Rhodpsn.	Matches	237; Conservative 24; Mismatches 35; Indels 12; Gaps 3;
PFam	PF00001; 7cm_1; 1.	QY	24 FDYDYG--APCHRFDVQIAQOLLPLPLSVFTGFYGNMLVYLINCKKLKCLTDIYL 81
PROSITE	PS000196; COPPER_BLU; UNKNOWN_1.	Db	3 YDIDGSEPERCKIDWQMGAHLLPLPSMFLFGFGNMLVVLINCKRPSMTDIYL 62
PROSITE	PS00237; G_PROTEIN_RECV_F1_1; UNKNOWN_1.	QY	82 LNLAISDILFLITLPLWAHSAANNEWYGNAMCKLFTGSLHYFGGIFTILLTIDRYLA 141
DR	PROSITE; PS50262; G_PROTEIN_RECV_F1_2; 1.	Db	63 LNLAISDILFLITVTPWYAAQGQWDGNTMCQFLTLYFGEFFSGLITLTIDRYLA 122
RW	Receptor.	QY	142 IVHAVALPKARVTVFGVTVTSVTLWVAFASVPGFLITKQKEDSVYVCGPYFPRG --- 197
SEQUENCE	352 AA; 40440 MW; FOA666CB4FE3964B CRC64;	Db	123 IVHAVALPKARVTVFGVTVTSVTLWVAFASVPGFLITRSGKLYTCSYPFGYQF 182
DR	Best Local Similarity 76.6%; Score 1243; DB 6; Length 352;	QY	198 WNNFTHTIMRNLLGVLVFLLLWVYCSGILKTLLRCLRNKKHRRAVFTIMIVYFLWT 257
DR	Matches 236; Conservative 27; Mismatches 33; Indels 12; Gaps 3;	Db	183 WKNFTETLKMVILGLVPLLLINVTCVSGILKTLLRCLRNKKHRRAVFTIMIVYFLWA 242
QY	24 FDYDYGA--PCHKFDVQIGAQQLPLPLSVLYFICFGVGNMLVVLINCKKLKCLTDIYL 81	QY	258 PYNIVLILNFTQEFFGINSCESTSQLDQATOVTETLGMTHCCINPITYAFGEKFRSLF - 316
Db	10 YDIDGASEPERCKTDVKQMSAHLPLPSMFLFGFGNMLVVLINCKRPSMTDIYL 69	Db	243 PYNIVLILNFTQEFFGILNCSNSNRLQAMQVTETLGMTHCCVNPNTIYAFGEKFRNLV 302
QY	82 LNLAISDILFLITLPLWAHSAANNEWYGNAMCKLFTGSLHYFGGIFTILLTIDRYLA 141	RESULT	8
Db	70 LNLAISDILFLITVTPWYAAQGQWDGNTMCQFLTLYFGEFFSGLITLTIDRYLA 129	Q9M299	PRELIMINARY; PRT; 352 AA.
QY	142 IVHAVALPKARVTVFGVVTSTVTLWVAFASVPGFLITKQKEDSVYVCGPYFPRG --- 197	Q9M299	SEQUENCE FROM N.A.
Db	130 IVHAVALPKARVTVFGVMTSVTWWVAVASLPLGIFTTSQEGYHYTOSPHFFGQYQF 189	AC	Q9M299; PRT; 352 AA.
QY	198 WNNFTHTIMRNLLGVLVFLLLWVYCSGILKTLLRCLRNKKHRRAVFTIMIVYFLWT 257	DT	PubMed=10747879;
Db	190 WKNFTETLKVIGLVLPLMVICYSGILKTLLRCLNEKKHRRAVFTIMIVYFLWT 257	RA	Munimdi S., Bamshad M., Ahuja S.S., Gonzalez E., Feuillet P.M., Begum K., Galvis M.C., Kostecki V., Valente A.J., Murthy K.K., Haro L., Dolan M.J., Allan J.S., Ahuja S.K.
QY	258 PYNIVLILNFTQEFFGINSCESTSQLDQATOVTETLGMTHCCINPITYAFGEKFRSLF - 316	RT	"Evolution of human and non-human primate CC chemokine receptor 5 gene and mRNA. Potential roles for haplotype and mRNA diversity, differential haplotype-specific transcriptional activity, and altered transcription factor binding to polymorphic nucleotides in the pathogenesis of HIV-1 and simian immunodeficiency virus."
Db	310 VFFQKHLA 310	DE	J. Biol. Chem. 275:18946-18961 (2000).
OS	Atelopus sp. (Spider monkey), Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Primates; Platyrrhini; Cebidae; Atelinae; Atelopus.	DR	EMBL; AF252555; AAF87935; 1.
OC	Atelopus sp.	DR	InterPro; IPR00923; BlueCn_1.
OC	Eutheria; Primates; Platyrrhini.	DR	InterPro; IPR00276; GPCR_Rhodpsn.
OC	Mammalia; Chordata; Craniata; Vertebrata; Euteleostomi;	DR	PF00001; 7cm_1; 1.
RN	SEQUENCE FROM N.A.	RT	"Sequences of the CCR5 genes from diverse simian and prosimian
RP	Konstam K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,	RT	
RA	Shibata R., Yoder A., Pillai S., Kuhlen C., Marx P., Wolinsky S.,	RT	
RT	"Sequences of the CCR5 genes from diverse simian and prosimian	RT	

Qy 198 WNNFTIMRNLLGLVPLLIVCYSGLKTLLCRNEKKRHRAYRIFTIMIVYFLFWT 257
 Db 183 WKNFETLKMVIGVPLLIVCYSGLKTLLCRNEKKRHRAYRIFTIMIVYFLFWA 242
 Qy 258 PYNTVLLNTFQEFFGLNSCNESTSQDQATOVTETLGMTCCINPIYAFGEKERSLF- 316
 Db 243 PYNTVLLNTFQEFFGLNSCNESTSQDQATOVTETLGMTCCVNPNTIYAFGEKERNLY 302
 Qy 317 ----HIA 319
 Db 303 VFFOKHIA 310

RESULT 11
 Q9TUUV9 PRELIMINARY; PRT; 339 AA.
 ID Q9TUUV9; PRELIMINARY; PRT; 339 AA.
 AC 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 ID 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 AC C-C chemokine receptor 5 (Fragment).
 RT CCR5.
 OS Hylobates concolor (crested gibbon)
 OC Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
 OC NCBI_TAXID=29089;
 RN 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
 RP SEQUENCE FROM N.A.
 RA Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
 RA "Sequences of the CCR5 genes from diverse simian and prosimian
 RA species.";
 RA Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF161928; ADD779_1; -.
 DR InterPro; IPR00923; BlueCu_1.
 DR InterPro; IPR00276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCR_RHODOPSN.
 DR PROSITE; PS00237; G-PROTEIN RECEP_F1_1; UNKNOWN_1.
 DR PROSITE; PS50262; G-PROTEIN RECEP_F1_2; 1.
 DR NON_TER 339 AA; 39051 MW; 5555PEAF2614D35C CRC64;
 DR PROSITE; PS50262; G-PROTEIN RECEP_F1_2; 1.
 KW Receptor.
 FT NON_TER 1
 SQ SEQUENCE 339 AA; 39051 MW; 5555PEAF2614D35C CRC64;
 DR DYYDGPCKIKEDYKQIGAQGLLPPPLSIFIEFGVNMLYVLLINCKLKCLDTIYLNL 84
 DR 6 DYDGPCKIKYQTAARLPLSIFIEFGVNMLYVLLINCKLKSMTDIYLNL 65

Query Match 62.7%; Score 1236; DB 6; Length 339;
 Best Local Similarity 77.4%; Pred. No. 3.e-101;
 Matches 236; Conservative 25; Mismatches 34; Indels 10; Gaps 2;

Qy 25 AIDSLFLITPLWAHSANNEWVFGNAMCKLFLPGLYHICFGGLFFLTLTIDYLAIVH 144
 Db 66 AIDSLFLITLTPWAHAAAQDFGNTMCQQLTGLYFIGGFSGLIFFLTIDYLAIVH 125

Qy 145 AVFALKARTVTVGTVVTSVTVLVAEVASPGIIFTKQREDSYVCGPYFP---RCWNN 200
 Db 126 AVFALKARTVTSVTVVAVFASLPGIIFTRSQEGHLHTCSSHPEPSYQFWKN 185

Qy 85 AIDSLFLITPLWAHSANNEWVFGNAMCKLFLPGLYHICFGGLFFLTLTIDYLAIVH 144
 Db 66 AIDSLFLITLTPWAHAAAQDFGNTMCQQLTGLYFIGGFSGLIFFLTIDYLAIVH 125

Qy 145 AVFALKARTVTVGTVVTSVTVLVAEVASPGIIFTKQREDSYVCGPYFP---RCWNN 200
 Db 126 AVFALKARTVTSVTVVAVFASLPGIIFTRSQEGHLHTCSSHPEPSYQFWKN 185

Qy 201 FHTIMRNLLGLVPLLIVCYSGLKTLLCRNEKKRHRAYRIFTIMIVYFLFWY 260
 Db 186 FQTLKTVLGLVPLLIVCYSGLKTLLCRNEKKRHRAYRIFTIMIVYFLFWY 245

Qy 261 TYLLNFTQEFFGLNSCNESTSQDQATOVTETLGMTCCINPIYAFGEKERSLF--- 316
 Db 246 TYLLNFTQEFFGLNSCNESTSQDQATOVTETLGMTCCINPIYAFGEKERSLF--- 316

RESULT 13
 Q9TSN3
 ID Q9TSN3
 AC Q9TSN3
 RT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 ID 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 AC C-C chemokine receptor 5 (Fragment).
 RT CCR5.

Best Local Similarity	Conservative	Pred.	No.	5.5e-101;	Matches	236;	Mismatches	25;	Indels	12;	Caps	3;
Qy	24	FDYDGG--	ACCHKEFVKQJQAOQLLPLYSVLFISFGVGNMIVVLLILINCCKLKCLTDIYL	81								
Db	3	YDIDYGPSECRKIDVKQMAHLLPLYSVFLFGVGNMIVVLLILINCRRPKSMIDYL		62								
Qy	82	LNLALSDLILFLITLPLWAHSAANEWVFGNAMCKLETFGLYHIGYFGGIFTILLTDIYL		141								
Db	63	LNLALSDLILFLITLPLWAHSAANEWVFGNAMCKLETFGLYHIGYFGGIFTILLTDIYL		122								
Qy	142	IVHAFALKARTVTFGVVTSVITWLVAVPSPVGLIFTKQREDSYVVCGYFPRG	--	197								
Qy	142	IVHAFALKARTVTFGVVTSVITWLVAVPSPVGLIFTKQREDSYVVCGYFPRG	--	197								
Db	123	IVHAFALKARTVTFGVVTSVITWLVAVPSPVGLIFTKQREDSYVVCGYFPRG	--	182								
Qy	198	WNNHTIMNTLIGVPLLLIVCYSGILKLLRNRNEKRRAVTRVFTIMIYFLFWT		257								
Db	183	WKNFETLKMVPLGLVPLLIVCYSGILKLLRNRNEKRRAVTRVFTIMIYFLFWA		242								
Qy	258	PYNVILLNTFQEFGGLSNCESTSQLDQATQVTEFLGMTHCCINPITYAVGEKERSLF		316								
Db	243	PYNVILLNTFQEFGGLSNCESTSQLDQATQVTEFLGMTHCCINPITYAVGEKERSLF		302								
Qy	317	-----HIA	319									
Db	303	VFFQKHIA	310									

Search completed: May 19, 2003, 16:48:11
 Job time : 57.5586 secs